

SEQUENCE LISTING

ATTACH
TO
#4

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gary S. Gray et al.
- (ii) TITLE OF INVENTION: CTLA-4-Cy4 Fusion Proteins (As Amended)
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 28 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: Not yet available
 - (B) FILING DATE: December 20, 2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/227,595
 - (B) FILING DATE: January 8, 1999
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Amy E. Mandragouras
 - (B) REGISTRATION NUMBER: 36,207
 - (C) REFERENCE/DOCKET NUMBER: RPN-001CN
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10027075.122001

CATTCTAGAA CCTCGACAAG CTTGAGATCA CAGTTCTCTC TAC

43

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCAGGCTG GGCCACGTGC ATTGCGGAGT GGACACCTGT GGAGAG

46

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTCCACAG GTGTCCACTC CGCAATGCAC GTGGCCCAGC CTGCTG

46

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGTGTGTGGA ATTCTCATTA CTGATCAGAA TCTGGGCACG GTTCTG

46

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10027075.122001

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCATTTTAAG CTTTTTCCTG ATCAGGAGCC CAAATCTTCT GACAAACTC ACACATCTCC 60

ACCGTCTCCA GGTAAGCC 78

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TAATACGACT CACTATAGGG 20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGCATTTTC CTGATCAGGA GTCCAAATAT GGTCCCCAC CCCATCATCC CCAGGTAAGC 60

CAACCC 66

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10027075.122001

GCAGAGGAAT TCGAGCTCGG TACCCGGGGA TCCCCAGTGT GGGGACAGTG GGACCCGCTC 60
TGCCTCCC 68

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTTTTGGG GGGAAGAGGA AGACTGACGG TGCCCCCTCG GCTTCAGGTG CTGAGGAAG 59

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATCTCTTCC TCAGCACCTG AAGCCGAGGG GGCACCGTCA GTCTTCCTCT TCCCCC 56

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCACGTGAC CTCAGGGGTC CGGGAGATCA TGAGAGTGTC CTTGGGTTTT GGGGGGAACA 60

GGAAGACTGA TGGTGCCCCC TCGAACTCAG GTGCTGAGG 99

(2) INFORMATION FOR SEQ ID NO:12:

10027075.122001

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCTCAGCACC TGAGTCGAG GGGGCACCAT CAGTCTTCCT GTTCCCCCA AAACCCAAGG 60

ACACTCTCAT GATCTCCCGG ACCCCTGAGG TCACGTGCG 99

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CATTCGCTTA CCTCGACAAG CTTGAGATCA CAGTTCTCTC TAC 43

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAGTGGACA CCTGTGGAGA G 21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCCACAGGT GTCCACTCCG CAATGCACGT GGCCCAGCC

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGTTGTAA GGACTCACCT GAAATCTGGG CTCCGTTGC

39

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCAACGGAGC CCAGATTTC A GGTGAGTCCT TACAACCTC

39

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCTAGATAT CTCTAGACTA TAAATCTCTG GCCATGAAG

39

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

10027075.122001

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCACTAGGT CGACTCTAGA AACTGAGGAA GCAAAGTTTA AATTCTACTC ACGTTTAATC 60

TGGGCTCCGT TGC 73

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCAGAGAGAC ATATGGCAAT GCACGTGGCC CAGCCTGCTG TGG 43

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGAGAGAG GATCCTCAGT CAGTTAGTCA GAATCTGGGC ACGGTTCTGG 50

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGCACTAGTC ATGAAATACC TATTGCCTAC GGCAGCCGCT GGATTGTTAT TACTCGCTGC	60
CCAACCAGCG ATGGCCGCAG CAATGCACGT GGCCAGCCT GCTGTGG	107

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC	540
CCAGATTTAT GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGC CCAAATCTTC	600
TGACAAAAC CACACATCTC CACCGTCTCC AGGTAAGCCA GCCCAGGCCT CGCCCTCCAG	660
CTCAAGGCGG GACAGGTGCC CTAGAGTAGC CTGCATCCAG GGACAGGCCC CAGCCGGGTG	720
CTGACACGTC CACCTCCATC TCTTCCTCAG CACCTGAAGC CGAGGGGGCA CCGTCAGTCT	780
TCCTCTTCCC CCCAAAACCC AAGGACACCC TCATGATCTC CCGGACCCCT GAGGTCACAT	840
GCGTGGTGGT GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG TACGTGGACG	900
GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC AGCACGTACC	960
GGGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT GAATGGCAAG GAGTACAAGT	1020

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GCAAGGTCTC CAACAAAGCC CTCCCAGCCC CCATCGAGAA AACCATCTCC AAAGCCAAAG 1080
 GTGGGACCCG TGGGGTGCGA GGGCCACATG GACAGAGGCC GGCTCGGCCC ACCCTCTGCC 1140
 CTGAGAGTGA CCGCTGTACC AACCTCTGTC CTACAGGGCA GCCCCGAGAA CCACAGGTGT 1200
 ACACCCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA GGTCAGCCTG ACCTGCCTGG 1260
 TCAAAGGCTT CTATCCCAGC GACATCGCCG TGGAGTGGGA GAGCAATGGG CAGCCGGAGA 1320
 ACAACTACAA GACCACGCCT CCCGTGCTGG ACTCCGACGG CTCCTTCTTC CTCTACAGCA 1380
 AGCTCACCGT GGACAAGAGC AGGTGGCAGC AGGGGAACGT CTTCTCATGC TCCGTGATGC 1440
 ATGAGGCTCT GCACAACCAC TACACGCAGA AGAGCCTCTC CCTGTCTCCG GGTAATGAG 1500
 TGCGACGGCC GGCAAGCCCC GCTCCCCGGG CTCTCGCGGT CGCACGAGGA TGCTTGGCAC 1560
 GTACCCCCTG TACATACTTC CCGGGCGCCC AGCATGGAAA TAAAGCACCC AGCGCTGCCC 1620
 TGGGCCCCCTG CGAGACTGTG ATGGTTCTTT CCACGGGTCA GGCCGAGTCT GAGGCCTGAG 1680
 TGGCATGAGG GAGGCAGAGC GGGTC 1705

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Gly	Tfp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	
Val	His	Ser	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser
			20					25					30		
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Ala	Ser	Pro	Gly	Lys
		35					40					45			
Ala	Thr	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Ala	Asp	Ser	Gln	Val
	50					55				60					
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe
65					70					75				80	
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn
				85					90					95	

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Leu Thr Ile	Gln Gly	Leu Arg	Ala Met	Asp Thr	Gly Leu	Tyr Ile	Cys
100			105			110	
Lys Val	Glu Leu	Met Tyr	Pro Pro	Pro Tyr	Tyr Leu	Gly Ile	Gly Asn
115			120			125	
Gly Thr	Gln Ile	Tyr Val	Ile Asp	Pro Glu	Pro Cys	Pro Asp	Ser Asp
130			135			140	
Gln Glu	Pro Lys	Ser Ser	Asp Lys	Thr His	Thr Ser	Pro Pro	Ser Pro
145		150			155		160
Ala Pro	Glu Ala	Glu Gly	Ala Pro	Ser Val	Phe Leu	Phe Pro	Pro Lys
	165			170			175
Pro Lys	Asp Thr	Leu Met	Ile Ser	Arg Thr	Pro Glu	Val Thr	Cys Val
	180			185			190
Val Val	Asp Val	Ser His	Glu Asp	Pro Glu	Val Lys	Phe Asn	Trp Tyr
	195		200			205	
Val Asp	Gly Val	Glu Val	His Asn	Ala Lys	Thr Lys	Pro Arg	Glu Glu
210			215			220	
Gln Tyr	Asn Ser	Thr Tyr	Arg Val	Val Ser	Val Leu	Thr Val	Leu His
225		230			235		240
Gln Asp	Trp Leu	Asn Gly	Lys Glu	Tyr Lys	Cys Lys	Val Ser	Asn Lys
	245			250			255
Ala Leu	Pro Ala	Pro Ile	Glu Lys	Thr Ile	Ser Lys	Ala Lys	Gly Gln
	260			265			270
Pro Arg	Glu Pro	Gln Val	Tyr Thr	Leu Pro	Pro Ser	Arg Asp	Glu Leu
	275		280			285	
Thr Lys	Asn Gln	Val Ser	Leu Thr	Cys Leu	Val Lys	Gly Phe	Tyr Pro
290			295			300	
Ser Asp	Ile Ala	Val Glu	Trp Glu	Ser Asn	Gly Gln	Pro Glu	Asn Asn
305		310			315		320
Tyr Lys	Thr Thr	Pro Pro	Val Leu	Asp Ser	Asp Gly	Ser Phe	Phe Leu
	325			330			335
Tyr Ser	Lys Leu	Thr Val	Asp Lys	Ser Arg	Trp Gln	Gln Gly	Asn Val
	340		345			350	
Phe Ser	Cys Ser	Val Met	His Glu	Ala Leu	His Asn	His Tyr	Thr Gln
	355		360			365	
Lys Ser	Leu Ser	Leu Ser	Pro Gly	Lys			
370			375				

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1747 base pairs

10027075.122001

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC	540
CCAGATTTAT GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGT CCAAATATGG	600
TCCCCATCC CCATCATCCC CAGGTAAGCC AACCAGGCC TCGCCCTCCA GCTCAAGGCG	660
GGACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC CCAGCCGGGT GCTGACGCAT	720
CCACCTCCAT CTCTTCCTCA GCACCTGAGT TCCTGGGGGG ACCATCAGTC TTCCTGTTCC	780
CCCCAAAACC CAAGGACACT CTCATGATCT CCCGGACCCC TGAGGTCACG TCGTGTTGG	840
TGGACGTGAG CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GCGTGAGG	900
TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC CGTGTTGGTCA	960
GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAACGGCAA GGAGTACAAG TGCAAGGTCT	1020
CCAACAAAGG CCTCCCGTCC TCCATCGAGA AAACCATCTC CAAAGCCAAA GGTGGGACCC	1080
ACGGGGTGCG AGGGCCACAC GGACAGAGGC CAGCTCGGCC CACCCTCTGC CCTGGGAGTG	1140
ACCGCTGTGC CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCCTG	1200
CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC	1260
TTCTACCCCA GCGACATCGC CGTGAGTGG GAGAGCAATG GGCAGCCGGA GAACAATACT	1320
AAGACCACGC CTCCCGTGCT GGACTCCGAC GGCTCCTTCT TCCTCTACAG CAGGCTAACC	1380
GTGGACAAGA GCAGGTGGCA GGAGGGGAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT	1440

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CTGCACAACC ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG 1500
 CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTCGCGCGA GGATGCTTGG CACGTACCCC 1560
 GTCTACATAC TTCCCAGGCA CCCAGCATGG AAATAAAGCA CCCACCACTG CCCTGGGCCC 1620
 CTGTGAGACT GTGATGGTTC TTTCCACGGG TCAGGCCGAG TCTGAGGCCT GAGTGACATG 1680
 AGGGAGGCAG AGCGGTCCCA CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT 1740
 CCTCTGC 1747

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	1	5	10	15
Val	His	Ser	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser	20	25	30	
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Ala	Ser	Pro	Gly	Lys	35	40	45	
Ala	Thr	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Ala	Asp	Ser	Gln	Val	50	55	60	
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe	65	70	75	80
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn	85	90	95	
Leu	Thr	Ile	Gln	Gly	Leu	Arg	Ala	Met	Asp	Thr	Gly	Leu	Tyr	Ile	Cys	100	105	110	
Lys	Val	Glu	Leu	Met	Tyr	Pro	Pro	Pro	Tyr	Tyr	Leu	Gly	Ile	Gly	Asn	115	120	125	
Gly	Thr	Gln	Ile	Tyr	Val	Ile	Asp	Pro	Glu	Pro	Cys	Pro	Asp	Ser	Asp	130	135	140	
Gln	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Ser	Pro	Ser	Ser	Pro	Ala	Pro	Glu	145	150	155	160
Phe	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	165	170	175	

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Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
180 185 190

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
195 200 205

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
210 215 220

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
225 230 235 240

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
245 250 255

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
260 265 270

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
275 280 285

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
290 295 300

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
305 310 315 320

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
325 330 335

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
340 345 350

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
355 360 365

Ser Leu Ser Leu Gly Lys
370

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1747 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGAAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480
CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC	540
CCAGATTTAT GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGT CCAAATATGG	600
TCCCCATCC CCATCATCCC CAGGTAAGCC AAGCCAGGCC TCGCCCTCCA GCTCAAGGCG	660
GGACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC CCAGCCGGGT GCTGACGCAT	720
CCACCTCCAT CTCTTCCTCA GCACCTGAGT TCGAGGGGGC ACCATCAGTC TTCCTGTTCC	780
CCCCAAAACC CAAGGACACT CTCATGATCT CCCGGACCCC TGAGGTCACG TCGTGTTGG	840
TGGACGTGAG CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GCGTGAGG	900
TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC CGTGTGGTCA	960
GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAACGGCAA GGAGTACAAG TGCAAGGTCT	1020
CCAACAAAGG CCTCCCGTCC TCCATCGAGA AAACCATCTC CAAAGCCAAA GGTGGGACCC	1080
ACGGGGTGCG AGGGCCACAC GGACAGAGGC CAGCTCGGCC CACCCTCTGC CCTGGGAGTG	1140
ACCGCTGTGC CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCCTG	1200
CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC	1260
TTCTACCCCA GCGACATCGC CGTGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACTAC	1320
AAGACCACGC CTCCCGTGCT GGAATCCGAC GGCTCCTTCT TCCTCTACAG CAGGCTAACC	1380
GTGGACAAGA GCAGGTGGCA GGAGGGGAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT	1440
CTGCACAACC ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG	1500
CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTCGCGCGA GGATGCTTGG CACGTACCCC	1560
GTCTACATAC TTCCCAGGCA CCCAGCATGG AAATAAAGCA CCCACCACTG CCCTGGGCCC	1620
CTGTGAGACT GTGATGGTTC TTTCCACGGG TCAGGCCGAG TCTGAGGCCT GAGTGACATG	1680
AGGGAGGCAG AGCGGTCCCA CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT	1740

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CCTCTGC

1747

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser
 20 25 30

Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys
 35 40 45

Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val
 50 55 60

Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
 65 70 75 80

Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn
 85 90 95

Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
 100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
 115 120 125

Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp
 130 135 140

Gln Glu Ser Lys Tyr Gly Pro Pro Ser Pro Ser Ser Pro Ala Pro Glu
 145 150 155 160

Phe Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 165 170 175

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 180 185 190

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
 195 200 205

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Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
210 215 220

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
225 230 235 240

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
245 250 255

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
260 265 270

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
275 280 285

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
290 295 300

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
305 310 315 320

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
325 330 335

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
340 345 350

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
355 360 365

Ser Leu Ser Leu Gly Lys
370

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300

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TGAGGTCCGG	GTGACAGTGC	TTCGGCAGGC	TGACAGCCAG	GTGACTGAAG	TCTGTGCGGC	360
AACCTACATG	ATGGGGAATG	AGTTGACCTT	CCTAGATGAT	TCCATCTGCA	CGGGCACCTC	420
CAGTGGAAT	CAAGTGAACC	TCACTATCCA	AGGACTGAGG	GCCATGGACA	CGGGACTCTA	480
CATCTGCAAG	GTGGAGCTCA	TGTACCCACC	GCCATACTAC	CTGGGCATAG	GCAACGGAGC	540
CCAGATTTCA	GGTGAGTCCT	TACAACCTCT	CTCTTCTATT	CAGCTTAAAT	AGATTTTACT	600
GCATTTGTTG	GGGGGGAAT	GTGTGTATCT	GAATTTGAGG	TCATGAAGGA	CTAGGGACAC	660
CTTGGGAGTC	AGAAAGGGTC	ATTGGGAGCC	CGGGCTGATG	CAGACAGACA	TCCTCAGCTC	720
CCAGACTTCA	TGGCCAGAGA	TTTATAGTCT	AGAGGATCCC	CAGCTTTCTG	GGGCAGGCCA	780
GGCCTGACCT	TGGCTTTGGG	GCAGGGAGGG	GGCTAAGGTG	AGGCAGGTGG	CGCCAGCAGG	840
TGCACACCCA	ATGCCCATGA	GCCCAGACAC	TGGACGCTGA	ACCTCGCGGA	CAGTTAAGAA	900
CCCAGGGGCC	TCTGCGCCTG	GGCCAGCTC	TGTCCACAC	CGCGGTCACA	TGGCACCACC	960
TCTCTTGAG	CCTCCACCAA	GGGCCCATCG	GTCTTCCCCC	TGGCACCTC	CTCCAAGAGC	1020
ACCTCTGGGG	GCACAGCGGC	CCTGGGCTGC	CTGGTCAAGG	ACTACTTCCC	CGAACCAGGTG	1080
ACGGTGTCGT	GGAAGTCAGG	CGCCCTGACC	AGCGGCGTGC	ACACCTTCCC	GGCTGTCCTA	1140
CAGTCCTCAG	GACTCTACTC	CCTCAGCAGC	GTGGTGACCG	TGCCCTCCAG	CAGCTTGGGC	1200
ACCCAGACCT	ACATCTGCAA	CGTGAATCAC	AAGCCCAGCA	ACACCAAGGT	GGACAAGAAA	1260
GTTGGTGAGA	GGCCAGCACA	GGGAGGGAGG	GTGTCTGCTG	GAAGCAGGCT	CAGCGCTCCT	1320
GCCTGGACGC	ATCCCGGCTA	TGCAGCCCCA	GTCCAGGGCA	GCAAGGCAGG	CCCCGTCTGC	1380
CTCTTCACCC	GGAGCCTCTG	CCCGCCCCAC	TCATGCTCAG	GGAGAGGGTC	TTCTGGCTTT	1440
TTCCAGGCT	CTGGGCAGGC	ACAGGCTAGG	TGCCCCTAAC	CCAGGCCCTG	CACACAAAGG	1500
GGCAGGTGCT	GGGCTCAGAC	CTGCCAAGAG	CCATATCCGG	GAGGACCCTG	CCCCTGACCT	1560
AAGCCCACCC	CAAAGGCCAA	ACTCTCCACT	CCCTCAGCTC	GGACACCTTC	TCTCCTCCCA	1620
GATTCCAGTA	ACTCCCAATC	TTCTCTCTGC	AGAGCCCCAA	TCTTGTGACA	AAACTCACAC	1680
ATGCCACCG	TGCCCAGGTA	AGCCAGCCCA	GGCCTCGCCC	TCCAGCTCAA	GGCGGGACAG	1740
GTGCCCTAGA	GTAGCCTGCA	TCCAGGGACA	GGCCCCAGCC	GGGTGCTGAC	ACGTCCACCT	1800
CCATCTCTTC	CTCAGCACCT	GAATCCTGG	GGGGACCGTC	AGTCTTCCTC	TTCCCCCCTA	1860
AACCCAAGGA	CACCCTCATG	ATCTCCCGGA	CCCCTGAGGT	CACATGCGTG	GTGGTGACG	1920
TGAGCCACGA	AGACCCTGAG	GTCAAGTTCA	ACTGGTACGT	GGACGGCGTG	GAGGTGCATA	1980
ATGCCAAGAC	AAAGCCGCGG	GAGGAGCAGT	ACAACAGCAC	GTACCGGGTG	GTCAGCGTCC	2040

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TCACCGTCCT GCACCAGGAC TGGCTGAATG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA 2100
AAGCCCTCCC AGCCCCCATC GAGAAAACCA TCTCCAAAGC CAAAGGTGGG ACCCGTGGGG 2160
TGCGAGGGCC ACATGGACAG AGGCCGGCTC GGGCCACCCT CTGCCCTGAG AGTGACCGCT 2220
GTACCAACCT CTGTCCTACA GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT 2280
CCCGGGATGA GCTGACCAAG AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC 2340
CCAGCGACAT CGCCGTGGAG TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA 2400
CGCCTCCCGT GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA 2460
AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA 2520
ACCACTACAC GCAGAAGAGC CTCTCCCTGT CTCCGGGTAA ATGAGTGCGA CGGCCGGCAA 2580
GCCCCGCTCC CCGGGCTCTC GCGGTCGCAC GAGGATGCTT GGCACGTACC CCCTGTACAT 2640
ACTTCCCGGG CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAGA 2700
CTGTGATGGT TCTTTCCACG GGTGAGGCCG AGTCTGAGGC CTGAGTGGCA TGAGGGAGGC 2760
AGAGCGGGTC 2770

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1				5					10					15	
Val	His	Ser	Ala	Met	His	Val	Ala	Gln	Pro	Ala	Val	Val	Leu	Ala	Ser
			20					25					30		
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val	Cys	Glu	Tyr	Ala	Ser	Pro	Gly	Lys
		35					40					45			
Ala	Thr	Glu	Val	Arg	Val	Thr	Val	Leu	Arg	Gln	Ala	Asp	Ser	Gln	Val
	50					55				60					
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr	Met	Met	Gly	Asn	Glu	Leu	Thr	Phe
65					70					75				80	
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly	Thr	Ser	Ser	Gly	Asn	Gln	Val	Asn
				85					90					95	

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Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys
 100 105 110

Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn
 115 120 125

Gly Ala Gln Ile Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 130 135 140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
 145 150 155 160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
 165 170 175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
 180 185 190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
 195 200 205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
 210 215 220

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1708 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTCGCTTA C�TCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT GAGCACACAG	60
GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTAAG	120
GGGCTCACAG TAGCAGGCTT GAGGTCTGGA CATATATATG GGTGACAATG ACATCCACTT	180
TGCCTTTCTC TCCACAGGTG TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT	240
GGCCAGCAGC CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC	300
TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG TCTGTGCGGC	360
AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC	420
CAGTGGAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA	480

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CATCTGCAAG GTGGAGCTCA TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAGC	540
CCAGATTAAA CGTGAGTAGA ATTTAAACTT TGCTTCCTCA GTTTCTAGAA GAATGGCTGC	600
AAAGAGCTCC AACAAAACAA TTTAGAACTT TATTAAGGAA TAGGGGGAAG CTAGGAAGAA	660
ACTCAAAACA TCAAGATTTT AAATACGCTT CTTGGTCTCC TTGCTATAAT TATCTGGGAT	720
AAGCATGCTG TTTTCTGTCT GTCCCTAACA TGCCCTGTGA TTATCCGCAA ACAACACACC	780
CAAGGGCAGA ACTTTGTTAC TTAAACACCA TCCTGTTTGC TTCTTTCCTC AGGAACTGTG	840
GCTGCACCAT CTGTCTTCAT CTTCCCGCCA TCTGATGAGC AGTTGAAATC TGGAAGTACC	900
TCTGTTGTGT GCCTGCTGAA TAACTTCTAT CCCAGAGAGG CCAAAGTACA GTGGAAGGTG	960
GATAACGCCC TCCAATCGGG TAACTCCCAG GAGAGTGTCA CAGAGCAGGA CAGCAAGGAC	1020
AGCACCTACA GCCTCAGCAG CACCTGACG CTGAGCAAAG CAGACTACGA GAAACACAAA	1080
GTCTACGCCT GCGAAGTCAC CCATCAGGGC CTGAGCTCGC CCGTCACAAA GAGCTTCAAC	1140
AGGGGAGAGT GTTAGAGGGA GAAGTGCCCC CACCTGCTCC TCAGTTCCAG CCTGACCCCC	1200
TCCCATCCTT TGGCCTCTGA CCCTTTTTC ACAGGGGACC TACCCCTATT GCGGTCCTCC	1260
AGCTCATCTT TCACCTCACC CCCCTCCTCC TCCTGGCTT TAATTATGCT AATGTTGGAG	1320
GAGAATGAAT AAATAAAGTG AATCTTTGCA CCTGTGGTTT CTCTCTTTC TCAATTTAAT	1380
AATTATTATC TGTTGTTTAC CAACTACTCA ATTTCTCTTA TAAGGGACTA AATATGTAGT	1440
CATCCTAAGG CGCATAACCA TTTATAAAAA TCATCCTTCA TTCTATTTTA CCCTATCATC	1500
CTCTGCAAGA CAGTCCTCCC TCAAACCCAC AAGCCTTCTG TCCTCACAGT CCCCTGGGCC	1560
GTGGTAGGAG AGACTTGCTT CCTTGTTTTC CCCTCCTCAG CAAGCCCTCA TAGTCCTTTT	1620
TAAGGGTGAC AGGTCTTACG GTCATATATC CTTTGATTCA ATTCCCTGGG AATCAACCAA	1680
GGCAAATTTT TCAAAAGAAG AAACCTGC	1708

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

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1		5		10		15	
Val	His	Ser	Ala	Met	His	Val	Ala
			20				25
							30
Ser	Arg	Gly	Ile	Ala	Ser	Phe	Val
		35				40	
							45
Ala	Thr	Glu	Val	Arg	Val	Thr	Val
	50				55		60
Thr	Glu	Val	Cys	Ala	Ala	Thr	Tyr
65					70		75
							80
Leu	Asp	Asp	Ser	Ile	Cys	Thr	Gly
				85			90
							95
Leu	Thr	Ile	Gln	Gly	Leu	Arg	Ala
			100				105
							110
Lys	Val	Glu	Leu	Met	Tyr	Pro	Pro
	115					120	
							125
Gly	Ala	Gln	Ile	Thr	Val	Ala	Ala
	130					135	
							140
Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
145					150		155
							160
Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
				165			170
							175
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
			180				185
							190
Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser
	195					200	
							205
Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr
	210					215	
							220
Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser
225						230	
							235

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